

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/533,299
Source: pcr
Date Processed by STIC: 6/30/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/533,299</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input checked="" type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input checked="" type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 <input checked="" type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text .	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules , each n or Xaa can only represent a single residue . Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)	
11 <input checked="" type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules <u>13,14,15,16,17</u>	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/533,299

DATE: 06/30/2006
TIME: 08:27:09

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06302006\J533299.raw

see item 4 on Error
summary sheet; also, see
item 2
on
Error
Sheet

4 <110> APPLICANT: Pieris Proteolab AG
6 <120> TITLE OF INVENTION: Soluble truncated polypeptides of the Nogo-A protein,
methods for the
7 production of such polypeptides and methods for identifying compounds having
8 detectable affinity to a Nogo-A protein
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/533,299
C--> 10 <141> CURRENT FILING DATE: 2005-04-29
W--> 0 <130> FILE REFERENCE:
E--> 10 <160> NUMBER OF SEQ ID NOS: 18 (see p.12)

ERRORED SEQUENCES

12 <210> SEQ ID NO: 1
13 <211> LENGTH: 1163
14 <212> TYPE: PRT
15 <213> ORGANISM: Rattus norvegicus
17 <220> FEATURE:
18 <223> OTHER INFORMATION: rat Nogo-A protein
20 <400> SEQUENCE: 1
22 Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser Thr Asp
23 1 5 10 15
25 Ser Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr
26 20 25 30
28 Glu Pro Glu Asp Glu Glu Asp Glu Glu Glu Asp Glu Glu
29 35 40 45
31 Glu Asp Asp Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys
32 50 55 60
34 Pro Ala Ala Gly Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala
35 65 70 75
37 Ala Pro Leu Leu Asp Phe Ser Ser Asp Ser Val Pro Pro Ala Pro
38 80 85 90
40 Arg Gly Pro Leu Pro Ala Ala Pro Pro Ala Ala Pro Glu Arg Gln
41 95 100 105
43 Pro Ser Trp Glu Arg Ser Pro Ala Ala Pro Ala Pro Ser Leu Pro
44 110 115 120
46 Pro Ala Ala Ala Val Leu Pro Ser Lys Leu Pro Glu Asp Asp Glu
47 125 130 135
49 Pro Pro Ala Arg Pro Pro Pro Pro Pro Ala Gly Ala Ser Pro
50 140 145 150
52 Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro Lys
53 155 160 165
55 Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu Pro
56 170 175 180

see p.21
Does Not Comply
Corrected Diskette Needed

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PATENT APPLICATION: US/10/533,299

DATE: 06/30/2006
TIME: 08:27:09

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06302006\J533299.raw

58 Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu Lys Ile Met
59 185 190 195
61 Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly Gln Glu
62 200 205 210
64 Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser
65 215 220 225
67 Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu
68 230 235 240
70 Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu
71 245 250 255
73 Thr Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn
74 260 265 270
76 Pro Phe Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr
77 275 280 285
79 Ser Glu Met Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser
E--> 80 290 295 310 300
82 Ala Ile Leu Val Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser
83 305 310 315
85 Lys Asp Lys Glu Asp Leu Val Cys Ser Ala Ala Leu His Ser Pro
86 320 325 330
88 Gln Glu Ser Pro Val Gly Lys Glu Asp Arg Val Val Ser Pro Glu
89 335 340 345
91 Lys Thr Met Asp Ile Phe Asn Glu Met Gln Met Ser Val Val Ala
92 350 355 360
94 Pro Val Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe Glu Gln Ala
95 365 370 375
97 Trp Glu Val Lys Asp Thr Tyr Glu Gly Ser Arg Asp Val Leu Ala
98 380 385 390
100 Ala Arg Ala Asn Val Glu Ser Lys Val Asp Arg Lys Cys Leu Glu
101 395 400 405
103 Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp Ser Glu Gly Arg
104 410 415 420
106 Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro Val Lys Asp
107 425 430 435
109 Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser Ala Thr
110 440 445 450
112 Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His Thr
113 455 460 465
115 Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala
116 470 475 480
118 Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe
119 485 490 495
121 Leu Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp
122 500 505 510
124 Thr Leu Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu
125 515 520 525
127 Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu
128 530 535 540
130 Asn Glu Ala Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp

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Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06302006\J533299.raw

131	545	550	555
133	Leu Val Gln Thr Ser Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr		
134	560	565	570
136	Ala Gln Leu Cys Pro Ser Phe Glu Glu Ala Glu Ala Thr Pro Ser		
137	575	580	585
139	Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Leu		
140	590	595	600
142	Leu Pro Ser Ala Gly Ala Ser Val Val Gln Pro Ser Val Ser Pro		
143	605	610	615
145	Leu Glu Ala Pro Pro Pro Val Ser Tyr Asp Ser Ile Lys Leu Glu		
146	620	625	630
148	Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Asn Val Ala Leu		
149	635	640	645
151	Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu Pro Glu Ser Phe		
152	650	655	660
154	Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala		
155	665	670	675
157	Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro Ser Pro		
158	680	685	690
160	Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser Val		
161	695	700	705
163	Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu		
164	710	715	720
166	Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln		
167	725	730	735
169	Thr Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu		
170	740	745	750
172	Val Ser Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala		
173	755	760	765
175	Ser Pro Gln Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro		
176	770	775	780
178	Asn Leu His Ser Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr		
179	785	790	795
181	Leu Thr Lys Lys Glu Lys Ile Ser Leu Gln Met Glu Glu Phe Asn		
182	800	805	810
184	Thr Ala Ile Tyr Ser Asn Asp Asp Leu Leu Ser Ser Lys Glu Asp		
185	815	820	825
187	Lys Ile Lys Glu Ser Glu Thr Phe Ser Asp Ser Ser Pro Ile Glu		
188	830	835	840
190	Ile Ile Asp Glu Phe Pro Thr Phe Val Ser Ala Lys Asp Asp Ser		
191	845	850	855
193	Pro Lys Leu Ala Lys Glu Tyr Thr Asp Leu Glu Val Ser Asp Lys		
194	860	865	870
196	Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala Asp Ser Leu Pro Cys		
197	875	880	885
199	Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn Ile Tyr Pro Lys		
200	890	895	900
202	Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn Arg Ser Ser		
203	905	910	915

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205	Val	Ser	Lys	Ala	Ser	Ile	Ser	Pro	Ser	Asn	Val	Ser	Ala	Leu	Glu
206						920				925					930
208	Pro	Gln	Thr	Glu	Met	Gly	Ser	Ile	Val	Lys	Ser	Lys	Ser	Leu	Thr
209						935				940					945
211	Lys	Glu	Ala	Glu	Lys	Lys	Leu	Pro	Ser	Asp	Thr	Glu	Lys	Glu	Asp
212						950				955					960
214	Arg	Ser	Leu	Ser	Ala	Val	Leu	Ser	Ala	Glu	Leu	Ser	Lys	Thr	Ser
215						965				970					975
217	Val	Val	Asp	Leu	Leu	Tyr	Trp	Arg	Asp	Ile	Lys	Lys	Thr	Gly	Val
218						980				985					990
220	Val	Phe	Gly	Ala	Ser	Leu	Phe	Leu	Leu	Leu	Ser	Leu	Thr	Val	Phe
221						995				1000					1005
223	Ser	Ile	Val	Ser	Val	Thr	Ala	Tyr	Ile	Ala	Leu	Ala	Leu	Leu	Ser
224						1010				1015					1020
226	Val	Thr	Ile	Ser	Phe	Arg	Ile	Tyr	Lys	Gly	Val	Ile	Gln	Ala	Ile
E--> 227					1630	1025				1030					1035
229	Gln	Lys	Ser	Asp	Glu	Gly	His	Pro	Phe	Arg	Ala	Tyr	Leu	Glu	Ser
230						1040				1045					1050
232	Glu	Val	Ala	Ile	Ser	Glu	Glu	Leu	Val	Gln	Lys	Tyr	Ser	Asn	Ser
233						1055				1060					1065
235	Ala	Leu	Gly	His	Val	Asn	Ser	Thr	Ile	Lys	Glu	Leu	Arg	Arg	Leu
236						1070				1075					1080
238	Phe	Leu	Val	Asp	Asp	Leu	Val	Asp	Ser	Leu	Lys	Phe	Ala	Val	Leu
239						1085				1090					1095
241	Met	Trp	Val	Phe	Thr	Tyr	Val	Gly	Ala	Leu	Phe	Asn	Gly	Leu	Thr
242						1100				1105					1110
244	Leu	Leu	Ile	Leu	Ala	Leu	Ile	Ser	Leu	Phe	Ser	Ile	Pro	Val	Ile
245						1115				1120					1125
247	Tyr	Glu	Arg	His	Gln	Val	Gln	Ile	Asp	His	Tyr	Leu	Gly	Leu	Ala
248						1130				1135					1140
250	Asn	Lys	Ser	Val	Lys	Asp	Ala	Met	Ala	Lys	Ile	Gln	Ala	Lys	Ile
E--> 251						1145				41150					41155
253	Pro	Gly	Leu	Lys	Arg	Lys	Ala	Asp							
OK-> 254						1160									
258 <210>	SEQ ID NO:	2													
259 <211>	LENGTH:	1192													
260 <212>	TYPE:	PRT													
261 <213>	ORGANISM:	Homo sapiens													
263 <220>	FEATURE:														
264 <223>	OTHER INFORMATION:	human Nogo-A protein													
266 <400>	SEQUENCE:	2													
268	Met	Glu	Asp	Leu	Asp	Gln	Ser	Pro	Leu	Val	Ser	Ser	Ser	Asp	Ser
269 1						5				10					15
271	Pro	Pro	Arg	Pro	Gln	Pro	Ala	Phe	Arg	Tyr	Gln	Phe	Val	Arg	Glu
272						20				25					30
274	Pro	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Glu
275						35				40					45
277	Asp	Glu	Asp	Leu	Glu	Glu	Leu	Glu	Val	Leu	Glu	Arg	Lys	Pro	Ala
278						50				55					60

see
P.S.

*move numbers
directly under
first letter of
the amino
acid*

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280 Ala Gly Leu Ser Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly
 281 65 70 75
 283 Ala Pro Leu Met Asp Phe Gly Asn Glu Phe Val Pro Pro Ala Pro
 284 80 85 90
 286 Arg Gly Pro Leu Pro Ala Ala Pro Pro Val Ala Pro Glu Arg Gln
 287 95 100 105
 289 Pro Ser Trp Asp Pro Ser Pro Val Ser Ser Thr Val Pro Ala Pro
 290 110 115 120
 292 Ser Pro Leu Ser Ala Ala Ala Val Ser Pro Ser Lys Leu Pro Glu
 293 125 130 135
 295 Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro Pro Pro Ala Ser
 296 140 145 150
 298 Val Ser Pro Gln Ala Glu Pro Val Trp Thr Pro Pro Ala Pro Ala
 299 155 160 165
 301 Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro Lys Arg Arg Gly
 302 170 175 180
 304 Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu Pro Ala Ala
 305 185 190 195
 307 Ser Glu Pro Val Ile Arg Ser Ser Ala Glu Asn Met Glu Leu Lys
 308 200 205 210
 310 Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe Pro
 311 215 220 225
 313 Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro
 314 230 235 240
 316 Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Glu Asn Leu
 317 245 250 255
 319 Ser Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser
 320 260 265 270
 322 Glu Ala Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile
 323 275 280 285
 325 Asp Arg Asp Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met
 326 290 295 300
 328 Gly Ser Ser Phe Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile
 329 305 310 315
 331 Val Ala Asn Pro Arg Glu Glu Ile Ile Val Lys Asn Lys Asp Glu
 332 320 325 330
 334 Glu Glu Lys Leu Val Ser Asn Asn Ile Leu His Asn Gln Gln Glu
 335 335 340 345
 337 Leu Pro Thr Ala Leu Thr Lys Leu Val Lys Glu Asp Glu Val Val
 338 350 355 360
 340 Ser Ser Glu Lys Ala Lys Asp Ser Phe Asn Glu Lys Arg Val Ala
 E--> 341 365 370 385 395 375
 343 Val Glu Ala Pro Met Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe
 344 380 385 390
 346 Glu Arg Val Trp Glu Val Lys Asp Ser Lys Glu Asp Ser Asp Met
 347 395 400 405
 349 Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu Glu Ser Lys Val
 350 410 415 420
 352 Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr Asn His Glu

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Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06302006\J533299.raw

353	425	430	435
355 Lys Asn Ser Glu Ser Ser Asn Asp Asp	Thr Ser Phe Pro Ser	Thr	
356	440	445	450
358 Pro Glu Gly Ile Lys Asp Arg Pro Gly	Ala Tyr Ile Thr Cys	Ala	
359	455	460	465
361 Pro Phe Asn Pro Ala Ala Thr Glu Ser	Ile Ala Thr Asn Ile	Phe	
362	470	475	480
364 Pro Leu Leu Gly Asp Pro Thr Ser Glu	Asn Lys Thr Asp Glu	Lys	
365	485	490	495
367 Lys Ile Glu Glu Lys Lys Ala Gln Ile	Val Thr Glu Lys Asn	Thr	
368	500	505	510
370 Ser Thr Lys Thr Ser Asn Pro Phe Leu	Val Ala Ala Gln Glu	Ser	
371	515	520	525
373 Glu Thr Asp Tyr Val Thr Thr Asp Asn	Leu Thr Lys Val Thr	Glu	
374	530	535	540
376 Glu Val Val Ala Asn Met Pro Glu Gly	Leu Thr Pro Asp Leu	Val	
377	545	550	555
379 Gln Glu Ala Cys Glu Ser Glu Leu Asn	Glu Val Thr Gly Thr	Lys	
380	560	565	570
382 Ile Ala Tyr Glu Thr Lys Met Asp Leu	Val Gln Thr Ser Glu	Val	
383	575	580	585
385 Met Gln Glu Ser Leu Tyr Pro Ala Ala	Gln Leu Cys Pro Ser	Phe	
386	590	595	600
388 Glu Glu Ser Glu Ala Thr Pro Ser Pro	Val Leu Pro Asp Ile	Val	
389	605	610	615
391 Met Glu Ala Pro Leu Asn Ser Ala Val	Pro Ser Ala Gly Ala	Ser	
392	620	625	630
394 Val Ile Gln Pro Ser Ser Ser Pro Leu	Glu Ala Ser Ser Val	Gln	
395	635	640	645
397 Tyr Glu Ser Ile Lys His Glu Pro Glu	Asn Pro Pro Pro Tyr	Glu	
398	650	655	660
400 Glu Ala Met Ser Val Ser Leu Lys Lys	Val Ser Gly Ile Lys	Glu	
401	665	670	675
403 Glu Ile Lys Glu Pro Glu Asn Ile Asn	Ala Ala Leu Gln Glu	Thr	
404	680	685	690
406 Glu Ala Pro Tyr Ile Ser Ile Ala Cys	Asp Leu Ile Lys Glu	Thr	
407	695	700	705
409 Lys Leu Ser Ala Glu Pro Ala Pro Glu	Phe Ser Asp Tyr Ser	Glu	
410	710	715	720
412 Met Ala Lys Val Glu Gln Pro Val Pro	Asp His Ser Glu Leu	Val	
413	725	730	735
415 Glu Asp Ser Ser Pro Asp Ser Glu Pro	Val Asp Leu Phe Ser	Asp	
416	740	745	750
418 Asp Ser Ile Pro Asp Val Pro Gln Lys	Gln Asp Glu Thr Val	Met	
419	755	760	765
421 Leu Val Lys Glu Ser Leu Thr Glu Thr	Ser Phe Glu Ser Met	Ile	
422	770	775	780
424 Glu Tyr Glu Gln Lys Glu Lys Leu Ser	Ala Leu Pro Pro Glu	Gly	
425	785	790	795

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427 Gly Lys Pro Tyr Leu Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr
428 800 805 810
430 Lys Asp Thr Leu Leu Pro Asp Glu Val Ser Thr Leu Ser Lys Lys
431 815 820 825
433 Glu Lys Ile Pro Ile Gln Met Glu Glu Leu Ser Thr Ala Val Tyr
434 830 835 840
436 Ser Asn Asp Asp Leu Phe Ile Ser Lys Glu Ala Gln Ile Arg Glu
437 845 850 855
439 Thr Glu Thr Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu
440 860 865 870
442 Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp Ser Phe Ser Lys Leu
443 875 880 885
445 Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His Lys Ser Glu Ile
446 890 895 900
448 Ala Gln Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys Thr Glu Leu
449 905 910 915
451 Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val Glu Glu
452 920 925 930
454 Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala Thr
455 935 940 945
457 Ser Lys Val Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr
458 950 955 960
460 Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys
461 965 970 975
463 Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg
464 980 985 990
466 Ser Pro Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val
467 995 1000 1005
469 Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val
470 1010 1015 1020
472 Phe Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser
473 1025 1030 1035
475 Ile Val Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val
476 1040 1045 1050
478 Thr Ile Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln
479 1055 1060 1065
481 Lys Ser Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu
482 1070 1075 1080
484 Val Ala Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala
485 1085 1090 1095
487 Leu Gly His Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe
488 1100 1105 1110
490 Leu Val Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met
491 1115 1120 1125
493 Trp Val Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu
494 1130 1135 1140
496 Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr
497 1145 1150 1155
499 Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn

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Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06302006\J533299.raw

500 1160 1165 1170
 502 Lys Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro
 503 1175 1180 1185
 505 Gly Leu Lys Arg Lys Ala Glu
 506 1190
 723 <210> SEQ ID NO: 13
 724 <211> LENGTH: 2248
 725 <212> TYPE: DNA
 726 <213> ORGANISM: Artificial sequence
 728 <220> FEATURE:
 729 <221> NAME/KEY: sig_peptide
 730 <222> LOCATION: (22)...(84)
 732 <220> FEATURE:
 733 <221> NAME/KEY: mat_peptide
 734 <222> LOCATION: (85)...(2238)
 735 <223> OTHER INFORMATION: fusion protein of truncated rat Nogo-A fragment and Strep-tag II

(the entire sequence)
 this needs explanation to
 (2207-2237 section)
 see p. 11, too
 see item 11 on Euro summary
 sheet same error in seq. 14,
 15, 16, 17

737 <220> FEATURE:
 738 <221> NAME/KEY: CDS
 739 <222> LOCATION: (85)...(2208)
 740 <223> OTHER INFORMATION: mature truncated Nogo-A
 742 <220> FEATURE:
 743 <221> NAME/KEY: CDS
 744 <222> LOCATION: (2209)...(2238)
 745 <223> OTHER INFORMATION: Strep-tag II affinity tag
 748 <400> SEQUENCE: 13

752 tctagataac gagggcaaaa a atg aaa aag aca gct atc gcg att 45
 753 Met Lys Lys Thr Ala Ile Ala Ile
 754 -21 -20 -15
 756 gca gtg gca ctg gct ggt ttc gct acc gta gcg cag gcc tct ttt 90
 757 Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Ser Phe
 758 -10 -5 -1 1
 760 aaa gaa cat gga tac ctt ggt aac tta tca gca gtg tca tcc tca 135
 761 Lys Glu His Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser
 762 5 10 15
 764 gaa gga aca att gaa gaa act tta aat gaa gct tct aaa gag ttg 180
 765 Glu Gly Thr Ile Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu
 766 20 25 30
 768 cca gag agg gca aca aat cca ttt gta aat aga gat tta gca gaa 225
 769 Pro Glu Arg Ala Thr Asn Pro Phe Val Asn Arg Asp Leu Ala Glu
 770 35 40 45
 772 ttt tca gaa tta gaa tat tca gaa atg gga tca tct ttt aaa ggc 270
 773 Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe Lys Gly
 774 50 55 60
 776 tcc cca aaa gga gag tca gcc ata tta gta gaa aac act aag gaa 315
 777 Ser Pro Lys Gly Glu Ser Ala Ile Leu Val Glu Asn Thr Lys Glu
 778 65 70 75
 780 gaa gta att gtg agg agt aaa gac aaa gag gat tta gtt tgt agt 360
 781 Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp Leu Val Cys Ser
 782 80 85 90

RAW SEQUENCE LISTING
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DATE: 06/30/2006
TIME: 08:27:09

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06302006\J533299.raw

```

784 gca gcc ctt cac agt cca caa gaa tca cct gtg ggt aaa gaa gac 405
785 Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly Lys Glu Asp
786      95          100          105
788 aga gtt gtg tct cca gaa aag aca atg gac att ttt aat gaa atg 450
789 Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn Glu Met
790      110          115          120
792 cag atg tca gta gta gca cct gtg agg gaa gag tat gca gac ttt 495
793 Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp Phe
794      125          130          135
796 aag cca ttt gaa caa gca tgg gaa gtg aaa gat act tat gag gga 540
797 Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly
798      140          145          150
800 agt agg gat gtg ctg gct aga gct aat gtg gaa agt aaa gtg 585
801 Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val
802      155          160          165
804 gac aga aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg 630
805 Asp Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly
806      170          175          180
808 aag gat agt gaa ggc aga aat gag gat gct tct ttc ccc agt acc 675
809 Lys Asp Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr
810      185          190          195
812 cca gaa cct gtg aag gac agc tcc aga gca tat att acc tgt gct 720
813 Pro Glu Pro Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala
814      200          205          210
816 tcc ttt acc tca gca acc gaa agc acc aca gca aac act ttc cct 765
817 Ser Phe Thr Ser Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro
818      215          220          225
820 ttg tta gaa gat cat act tca gaa aat aaa aca gat gaa aaa aaa 810
821 Leu Leu Glu Asp His Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys
822      230          235          240
824 ata gaa gaa agg aag gcc caa att ata aca gag aag act agc ccc 855
825 Ile Glu Glu Arg Lys Ala Gln Ile Ile Thr Glu Lys Thr Ser Pro
826      245          250          255
828 aaa acg tca aat cct ttc ctt gta gca gta cag gat tct gag gca 900
829 Lys Thr Ser Asn Pro Phe Leu Val Ala Val Gln Asp Ser Glu Ala
830      260          265          270
832 gat tat gtt aca aca gat acc tta tca aag gtg act gag gca gca 945
833 Asp Tyr Val Thr Thr Asp Thr Leu Ser Lys Val Thr Glu Ala Ala
834      275          280          285
836 gtg tca aac atg cct gaa ggt ctg acg cca gat tta gtt cag gaa 990
837 Val Ser Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu
838      290          295          300
840 gca tgt gaa agt gaa ctg aat gaa gcc aca ggt aca aag att gct 1035
841 Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr Gly Thr Lys Ile Ala
842      305          310          315
844 tat gaa aca aaa gtg gac ttg gtc caa aca tca gaa gct ata caa 1080
845 Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser Glu Ala Ile Gln
846      320          325          330
848 gaa tca ctt tac ccc aca gca cag ctt tgc cca tca ttt gag gaa 1125

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```

849 Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser Phe Glu Glu
850      335          340          345
852 gct gaa gca act ccg tca cca gtt ttg cct gat att gtt atg gaa 1170
853 Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu
854      350          355          360
856 gca cca tta aat tct ctc ctt cca agc gct ggt gct tct gta gtg 1215
857 Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val Val
858      365          370          375
860 cag ccc agt gta tcc cca ctg gaa gca cct cct cca gtt agt tat 1260
861 Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
862      380          385          390
864 gac agt ata aag ctt gag cct gaa aac ccc cca cca tat gaa gaa 1305
865 Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu
866      395          400          405
868 gcc atg aat gta gca cta aaa gct ttg gga aca aag gaa gga ata 1350
869 Ala Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile
870      410          415          420
872 aaa gag cct gaa agt ttt aat gca gct gtt cag gaa aca gaa gct 1395
873 Lys Glu Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala
874      425          430          435
876 cct tat ata tcc att gcg tgt gat tta att aaa gaa aca aag ctc 1440
877 Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu
878      440          445          450
880 tcc act gag cca agt cca gat ttc tct aat tat tca gaa ata gca 1485
881 Ser Thr Glu Pro Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala
882      455          460          465
884 aaa ttc gag aag tcg gtg ccc gaa cac gct gag cta gtg gag gat 1530
885 Lys Phe Glu Lys Ser Val Pro Glu His Ala Glu Leu Val Glu Asp
886      470          475          480
888 tcc tca cct gaa tct gaa cca gtt gac tta ttt agt gat gat tcg 1575
889 Ser Ser Pro Glu Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser
890      485          490          495
892 att cct gaa gtc cca caa aca caa gag gag gct gtg atg ctc atg 1620
893 Ile Pro Glu Val Pro Gln Thr Gln Glu Glu Ala Val Met Leu Met
894      500          505          510
896 aag gag agt ctc act gaa gtg tct gag aca gta gcc cag cac aaa 1665
897 Lys Glu Ser Leu Thr Glu Val Ser Glu Thr Val Ala Gln His Lys
898      515          520          525
900 gag gag aga ctt agt gcc tca cct cag gag cta gga aag cca tat 1710
901 Glu Glu Arg Leu Ser Ala Ser Pro Gln Glu Leu Gly Lys Pro Tyr
902      530          535          540
904 tta gag tct ttt cag ccc aat tta cat agt aca aaa gat gct gca 1755
905 Leu Glu Ser Phe Gln Pro Asn Leu His Ser Thr Lys Asp Ala Ala
906      545          550          555
908 tct aat gac att cca aca ttg acc aaa aag gag aaa att tct ttg 1800
909 Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu Lys Ile Ser Leu
910      560          565          570
912 caa atg gaa gag ttt aat act gca att tat tca aat gat gac tta 1845
913 Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn Asp Asp Leu

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```

914      575          580          585
916 ctt tct tct aag gaa gac aaa ata aaa gaa agt gaa aca ttt tca 1890
917 Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr Phe Ser
918      590          595          600
920 gat tca tct ccg att gag ata ata gat gaa ttt ccc acg ttt gtc 1935
921 Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe Val
922      605          610          615
924 agt gct aaa gat gat tct cct aaa tta gcc aag gag tac act gat 1980
925 Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp
926      620          625          630
928 cta gaa gta tcc gac aaa agt gaa att gct aat atc caa agc ggg 2025
929 Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly
930      635          640          645
932 gca gat tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct ttc 2070
933 Ala Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe
934      650          655          660
936 aag aat ata tat cct aaa gat gaa gta cat gtt tca gat gaa ttc 2115
937 Lys Asn Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe
938      665          670          675
940 tcc gaa aat agg tcc agt gta tct aag gca tcc ata tcg cct tca 2160
941 Ser Glu Asn Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser
942      680          685          690
944 aat gtc tct gct ttg gaa cct cag aca gaa atg ggc agc ata gtt 2205
945 Asn Val Ser Ala Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val
946      695          700          705
948 aaa agc gct tgg cgt cac ccg cag ttc ggt ggt taa taa gctt 2248
E--> 949 Lys Ser Ala Trp Arg His Pro Gln Phe Gly Gly End (Delete - do not show anything)
950      710          715
955 <210> SEQ_ID NO: 14
956 <211> LENGTH: 2425
957 <212> TYPE: DNA needs explanation
958 <213> ORGANISM: Artificial sequence
960 <220> FEATURE:
961 <221> NAME/KEY: sig_peptide
962 <222> LOCATION: (22)...(84)
964 <220> FEATURE:
965 <221> NAME/KEY: mat_peptide ? There are only 2425 nucleotides in this sequence
966 <222> LOCATION: (85)...(2460) and in seq.15
967 <223> OTHER INFORMATION: fusion protein of truncated rat Nogo-A fragment and Strep-
tag II
969 <220> FEATURE:
970 <221> NAME/KEY: CDS
W--> 971 <222> LOCATION: (85)...(2430) ?
972 <223> OTHER INFORMATION: mature truncated Nogo-A
974 <220> FEATURE:
975 <221> NAME/KEY: CDS
W--> 976 <222> LOCATION: (2431)...(2460) ?
977 <223> OTHER INFORMATION: Strep-tag II affinity tag
980 <400> SEQUENCE: 14
983 tctagataac gagggcaaaa a atg aaa aag aca gct atc gcg att

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12

<210> 17
<211> 739
<212> PRT
<213> Artificial sequence

<220>
<221> SIGNAL
<222> (-21)...(-1)

<220>
<221> CHAIN
<222> (1)...(718)
<223> fusion protein of truncated rat Nogo-A fragment and Strep-tag II

<220>
<221>
<222> (1)...(708)
<223> mature truncated Nogo-A

<220>
<221>
<222> (709)...(718)
<223> Strep-tag affinity tag

<400> 17

last sequence in submitted file

this needs explanation in <220>-<223> section